

Claims

1. A β -fructofuranosidase variant consisting of the following amino acid sequence:

(a) a mutated amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues at positions 62, 122, 128, 165, 221, 395, and 550, or

(b) a mutated homologue of the amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues corresponding to the amino acid residues at positions 62, 122, 128, 165, 221, 395, and 550 of SEQ ID NO: 2.

2. The variant according to claim 1, wherein the mutation is a substitution.

3. The variant according to claim 2, wherein the substitution is

a substitution of the amino acid residue at position 62 with an acidic amino acid selected from the group consisting of aspartic acid and glutamic acid;

a substitution of the amino acid residue at position 122 with an amino acid selected from the group consisting of methionine, isoleucine, leucine, and valine;

a substitution of the amino acid residue at position 128 with an amino acid selected from the group consisting of asparagine and glutamine;

a substitution of the amino acid residue at position 165 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 221 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 395 with an amino acid selected from the group consisting of leucine, methionine, isoleucine, and valine; and

a substitution of the amino acid residue at position 550 with a hydroxy amino acid selected from the group consisting of serine and threonine.

4. The variant according to claim 1, 2, or 3, which further has a mutation in at least one amino acid residue at positions 170, 300, 313, and 386 of the amino acid sequence represented by SEQ ID NO: 2 and its homologue.

5. The variant according to claim 4, wherein the mutation is a substitution.

6. The variant according to claim 5, wherein the substitution is

a substitution of the amino acid residue at position 170 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 300 with an amino acid selected from the group consisting of tryptophan, phenylalanine, tyrosine, and valine;

a substitution of the amino acid residue at position 313 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine; and

a substitution of the amino acid residue at position 386 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine.

7. The variant according to claim 4, 5, or 6, which has mutations in the amino acid residues at positions 165, 300 and 313.

8. The variant according to claim 7, wherein the mutations are substitutions.

9. The variant according to claim 8, wherein the substitutions are

a substitution of the amino acid residue at position 165 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 300 with an amino acid selected from the group consisting of tryptophan, phenylalanine, tyrosine and valine; and

a substitution of the amino acid residue at position 313 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine.

10. A β -fructofuranosidase variant consisting of the following amino acid sequence:

(c) a mutated amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues at positions 40, 379, and 381, or

(d) a mutated homologue of the amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues corresponding to the amino acid residues at positions 40, 379, and 381 of SEQ ID NO: 2.

11. The variant according to claim 10, wherein the mutation is a substitution.

12. The variant according to claim 11, wherein the substitution is

a substitution of the amino acid residue at position 40 with an acidic amino acid selected from the group consisting of aspartic acid and glutamic acid;

a substitution of the amino acid residue at position 379 with cysteine; and

a substitution of the amino acid residue at position 381 with an amino acid selected from the group consisting of methionine, isoleucine, leucine, and valine.

13. A polynucleotide encoding the β -fructofuranosidase variant of any one of claims 1 to 12.

14. A recombinant vector comprising the polynucleotide of claim 13.

15. A transformant comprising the recombinant vector of claim 14.

16. A method for producing a fructooligosaccharide, which comprises the step of bringing the transformant of claim 15 or the β -fructofuranosidase variant of any one of claims 1 to 12 into contact with sucrose.